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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: December 15, 2002, 00:18:43 ; Search time 3175 seconds
1668.255 Million cell updates/sec

Title: US-09-762-105-14
Perfect score: 182
Sequence: 1 gggctgtccccgcgtc.....tgactggtagcaggttagc 182

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

1: gb-ba.*

2: gb-htg.*

3: gb-in.*

4: gb-on.*

5: gb-ov.*

6: gb-pi.*

7: gb-ph.*

8: gb-pl.*

9: gb-pr.*

10: gb-ro.*

11: gb-sts.*

12: gb-sy.*

13: gb-un.*

14: gb-vi.*

15: gb-wt.*

16: em-fun.*

17: em-hum.*

18: em-in.*

19: em-mu.*

20: em-or.*

21: em-ov.*

22: em-pat.*

23: em-pl.*

24: em-pl.*

25: em-pl.*

26: em-ro.*

27: em-sts.*

28: em-un.*

29: em-vi.*

30: em-htg-hum.*

31: em-htg-inv.*

32: em-htg-other.*

33: em-htg-sts.*

34: em-htg-pl.*

35: em-htg-rod.*

36: em-htg-nam.*

37: em-htg-vrt.*

38: em-sy.*

39: em-htgo-hum.*

40: em-htgo-mus.*

41: em-htgo-other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	182	100.0	5270	12	AF176637	AF176637 Plasmid t
C 2	111.2	61.1	168	6	AX076661	AX076661 Sequence
C 3	85.8	47.1	127	6	AX137514	AX137514 Sequence
C 4	85.8	47.1	127	6	E51179	E51179 Method for
C 5	85.8	47.1	127	6	E51197	E51197 Process for
C 6	85.8	47.1	766	8	TOBCPTCVR	J01453 Tobacco chl
C 7	85.8	47.1	2113	8	CHNTRN1	W00165 Tobacco chl
C 8	85.8	47.1	1778	8	CHNTRN1	X7938 R-plumbagin
C 9	85.8	47.1	7829	8	CHNTRN1	Y1938 R-plumbagin
C 10	85.8	47.1	155939	8	CHNTRN1	Z00044 Nicotiana t
C 11	85.8	47.1	155939	8	CHNTRN1	Z00044 Nicotiana t
C 12	85.8	47.1	156687	8	ABE316582	ABE316582 Atropa b
C 13	85.8	47.1	156687	8	ABE316582	ABE316582 Atropa b
C 14	85.4	46.9	184	6	ARI45914	ARI45914 Sequence
C 15	85.4	46.9	300	6	ARI17110	ARI17110 Sequence
C 16	85.4	46.9	300	6	ARI17110	ARI17110 Sequence
C 17	85.4	46.9	2962	12	XU12809	XU12809 Transform
C 18	85.4	46.9	3019	12	XU12811	XU12811 Transform
C 19	85.4	46.9	3019	12	XU12811	XU12811 Transform
C 20	85.4	46.9	3136	12	AF061065	AF061065 Plasmid t
C 21	85.4	46.9	4126	12	XU12814	XU12814 Transform
C 22	85.4	46.9	4126	12	XU12814	XU12814 Transform
C 23	85.4	46.9	4174	12	XU12812	XU12812 Transform
C 24	85.4	46.9	4174	12	XU12813	XU12813 Transform
C 25	85.4	46.9	4304	12	AY005806	AY005806 Transform
C 26	85.4	46.9	7454	12	CTR312391	AJ312391 Chloropla
C 27	85.4	46.9	7454	12	CTR312392	AJ312392 Chloropla
C 28	85.4	46.9	7454	12	CTR312393	AJ312393 Chloropla
C 29	84.8	46.6	159	12	M32201	M32201 Synthetic C
C 30	84.8	46.6	310	12	M32200	M32200 Synthetic C
C 31	84.8	46.6	2731	1	PET31F1P	XG4498 E.coli plas
C 32	84.8	46.6	2829	12	CVPRSET5C	X54204 Cloning vec
C 33	84.8	46.6	2829	12	CVPRSET6C	X54208 Cloning vec
C 34	84.8	46.6	2830	12	CVPRSET5B	X54203 Cloning vec
C 35	84.8	46.6	2830	12	CVPRSET6B	X54207 Cloning vec
C 36	84.8	46.6	2831	12	CVPRSET5A	X54202 Cloning vec
C 37	84.8	46.6	2831	12	CVPRSET6A	X54206 Cloning vec
C 38	84.8	46.6	2894	12	CVPRSET6A	U25269 Escherich
C 39	84.8	46.6	3984	6	IL15353	IL15353 Sequence 1
C 40	84.8	46.6	3993	12	CVPGEMEX1	X65317 Cloning vec
C 41	84.8	46.6	3995	12	CVPGEMEX2	X65318 Cloning vec
C 42	84.8	46.6	5231	6	AX001273	AX001273 Sequence
C 43	84.8	46.6	5953	6	AX191649	AX191649 Sequence
C 44	84.8	46.6	39937	7	F7CG	V01146 Genome of b
C 45	83.2	45.7	187	6	AR004778	AR004778 Sequence

ALIGNMENTS

RESULT 1
AF176637/c
LOCUS AF176637
DEFINITION Plasmid transformation vector pMSK49
VERSION AF176637
KEYWORDS Plasmid transformation vector pMSK49
SOURCE Plasmid transformation vector pMSK49
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 5270)
AUTHORS Khan,M.S. and Malliga,P.
TITLE Fluorescent antibiotic-resistance marker for tracking plasmid
transformation in higher plants
JOURNAL Nat. Biotechnol. 17 (9), 910-915 (1999)

[illegible]

QY	5	TGCGTCCCGCCGCGCTGCTCAATGAGATGGAATGAGAGCGCTGCTGGGATTCGACGTGAGG	64
DB	11	TTGCTGCCCGCCGCGCTGCTCAATGAGATGGAATGAGAGCGCTGCTGGGATTCGACGTGAGG	70
QY	65	GGCAGGATGGCTATATTTCTGGGAGGA	93
DB	71	GGCAGGATGGCTATATTTCTGGGAGGA	99
RESULT 5			
ES1197			
LOCUS	ES1197	127 bp	DNA
DEFINITION	Process for producing polyester.		
ACCESSION	ES1197		
VERSION	ES1197.1	GI:18629514	
KEYWORDS	JP 2001046074-A/16.		
SOURCE	Nicotiana tabacum		
ORGANISM	Nicotiana tabacum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; 1 (bases 1 to 127)		
AUTHORS	Nakashita, H., Yamauchi, I., Yoshioka, K. and Doi, Y.		
TITLE	Process for producing polyester		
JOURNAL	Patent: JP 2001046074-A 16 20-FEB-2001;		
COMMENT	RIKAGAKU KENRYUSHO		
FEATURES	Source		
BASE COUNT	28 a	24 c	45 g
ORIGIN			
LOCUS	ES1197	127 bp	DNA
DEFINITION	Method for transforming plant and transformed plant.		
ACCESSION	ES1197		
VERSION	ES1197.1	GI:18629496	
KEYWORDS	JP 2001046073-A/16.		
SOURCE	Nicotiana tabacum		
ORGANISM	Nicotiana tabacum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; 1 (bases 1 to 127)		
AUTHORS	Nakashita, H., Yamauchi, I., Yoshioka, K. and Doi, Y.		
TITLE	Method for transforming plant and transformed plant		
JOURNAL	Patent: JP 2001046073-A 16 20-FEB-2001;		
COMMENT	RIKAGAKU KENRYUSHO, HIDEO NAKASHITA		
BASE COUNT	28 a	24 c	45 g
ORIGIN			
LOCUS	ES1197	127 bp	DNA
DEFINITION	Method for transforming plant and transformed plant.		
ACCESSION	ES1197		
VERSION	ES1197.1	GI:18629496	
KEYWORDS	JP 2001046073-A/16.		
SOURCE	Nicotiana tabacum		
ORGANISM	Nicotiana tabacum		
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AUTHORS	Nakashita, H., Yamauchi, I., Yoshioka, K. and Doi, Y.		
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COMMENT	RIKAGAKU KENRYUSHO, HIDEO NAKASHITA		
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COMMENT	RIKAGAKU KENRYUSHO, HIDEO NAKASHITA		
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AUTHORS	Nakashita, H., Yamauchi, I., Yoshioka, K. and Doi, Y.		
TITLE	Method for transforming plant and transformed plant		
JOURNAL	Patent: JP 2001046073-A 16 20-FEB-2001;		
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BASE COUNT	28 a	24 c	45 g
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AUTHORS			

Query Match	Similarity	Score	DB 8:	Length	2113:
Matches	87	93.98	Pred. No. 1c-1e:		
Mismatches	0				
5	TCCTCCCGCCGCGTCAATGAAATAGAGAGGTCGTGGATTTCAGCTGAGG	64			
429	TTCTCTCCCGCCGCGTCAATGAAATAGAGAGGTCGTGGATTTCAGCTGAGG	488			
65	GCAGGAGTGGCTATATTCCTGGAGGA	93			
489	CTCTGATGTCGCGCTATATTCCTGGAGGA	517			

RESULT 8
CHNPTRNVI 3274 bp DNA linear PLN 04-JUN-1993
OCUS plumbaginifolia chloroplast 16S-DNA trnV and trnI genes for 16S
DEFINITION trnV and trnI genes for 16S
X70938.1. RNA, transfer RNA-val and transfer RNA-Ile 5' exon.
ACCESSION X70938.1 GI:14352
PERSON W70938.1
KEYWORDS 16S ribosomal RNA; inverted repeat; ribosomal RNA; transfer RNA;
transfer RNA-ile-gag; transfer RNA-val-gac; trnI gene; trnV gene.
SOURCE
ORGANISM plumbaginifolia
CULTURE cured-leaved tobacco
COLLECTION viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 2059 to 2418)
O'Neill, C.; Horvath, G.V.; Horvath, P.; Dill, P. J. and Medgyesy, P.
Chloroplast transformations in tobacco plants: polyethylene glycol (PEG)
systems
Journal of Protoplasts is an alternative to biolistic delivery
Plant J. 3 (5), 729-738 (1993)

```

AUTHORS      Horvath, G.V.
TITLE        Direct Submission
JOURNAL      Submitted (16-FEB-1993) G.V. Horvath, Biological Research Centre,
              Institute of Phys., Hungarian Academy of Science, PO Box 531
              5701 Szeged, HUNGARY
FEATURES     1. 3274
              Location/Qualifiers
                /organism="Nicotiana glauca"
                /strain="wild type"
                /db_xref="taxon:4092"
                /haplotype="diploid"
                /molecule="cDNA"
                /note="mature plant"
                /reftype="mature plant"
                /gene="trny"
                /gene="998"
                /gene="998"
                /product="RNA-Vai"
                /note="codon recognized: GAC"
                /anticodon="(pos:972..974,aa:val)
                1226..165=DNA"
                1226..2714
                /gene="16S=rRNA"
                /product="16S ribosomal RNA"
                /gene="trni"
                /gene="3015..3051"
                /gene="trni"
                /product="rRNA-ile"
                /note="5' exon"
                825 a 713 c 949 g 787 t
              47 18. score 85.8: DB 8: Length 3274:
              ORIGIN

```

Query Match

Submitted (27-FEB-1998) T. Toudouki, Data Processing Center,
Aichi University, 12-1 Taikwa, Iwasaki, Nishin, Aichi
466-8501, JAPAN

On or before Jan 17, 2002 this sequence version replaced g1:264799,
g1:11807

COMMENT

The circular tobacco chloroplast DNA sequence is presented in a
linearized form by cutting at the junction (JLA) between IRA and
JSC. JSC is designated zero and numbered proceeding towards LSC. The DNA
strand which codes for the large subunit of ribulose
1,5-bisphosphate carboxylase is designated as A strand and the
complementary strand as B strand. The sequence is presented.
Nucleotide sequence of region (LSC) 1 - 86686 (86686 bp) Inverted
repeat B (IRB) - 86687 - 112027 (25341 bp) Small single copy
region B (IRB) - 112028 - 130598 (18571 bp) Inverted repeat A
(IRA) - 130599 - 155939 (25341 bp) An alpha-tomato gene
chloroplast genes, and ORFs GENE NUCLEOTIDE NUMBER (FROM)
accD 112862
atpA 12148
atpB 56777
atpE 11452
atpH 14099
atpI 16000
clpP 74507
infA 83658
ndhA 123933
ndhB 99261, 143365
ndhC 52667
ndhD 119553
ndhE 114292
ndhG 120709
ndhH 125116
ndhI 51665
ndhJ 52425
orf70A 48941
orf70B 102102, 140524
orf74 10322, 131802
orf75 96556, 146070
orf92 96119, 146507
orf99 66176
orf103 57588
orf105 96407, 146219
orf111 102346, 140280
orf131 110229, 137776
orf350 104769, 137766
oriA 16435, 137606
oriB 177452
petA 79043
petB 68570
petG 43866
petL 41208
psaA 119389
psaC 52083
psaJ 57505
psbA 74953
psbB 35515
psbC 34470
psbD 67129
psbF 77101
psbI 8398

JOURNAL

REFERENCE

AUTHORS

TITLE

1. Michelon K. and Stephan J.
Fine structural features of the chloroplast genome: comparison of
the sequenced tobacco chloroplast genomes
Nucleic Acids Res. 19 (11), 3150 (1991)
1708498

2. Shimada, H. and Sugita, M.
Fine structural features of the chloroplast genome: comparison of
the sequenced tobacco chloroplast genomes
Nucleic Acids Res. 19 (5), 983-995 (1991)
9121240

3. Michelon K. and Stephan J.
Fine structural features of the chloroplast genome: comparison of
the sequenced tobacco chloroplast genomes
Nucleic Acids Res. 19 (11), 3150 (1991)
91279477

4. Sugita M. and Shimada H.
Fine structural features of the chloroplast genome: comparison of
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5. Sugita M. and Shimada H.
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Fine structural features of the chloroplast genome: comparison of
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Fine structural features of the chloroplast genome: comparison of
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91279477

41. Sugita M. and Shimada H.
Fine structural features of the chloroplast genome: comparison of
the sequenced tobacco

Mon Dec 16 13:20:21 2002

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Db      2  GCTCCGCCCGCTGTCATGAGATGATGAAGAGGCTGCTGGGATTGACGTGAGGGG 61
Oy      67  CAGGATGGCTATATTTCTGGAGGCA 93
Db      62  CAGGATGGCTATATTTCTGGAGGCA 88

RESULT 15
ARI71710  ARI71710 300 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6297054.
ACCESSION ARI71710
VERSION ARI71710.1 GI:17910660
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 300)
AUTHORS Maliga,P., Carrer,H. and Chaudhuri,S.
JOURNAL Nature Biotechnology
JOURNAL Patent: US 6297054-A 4 02-OCT-2001;
FEATURES             Location/Qualifiers
     source            1..300
                        /organism="unknown"
BASE COUNT    90 a      61 t
                63 c
                86 g

Query Match: 46.9%; Score 85.4; DB 6; Length 300;
Best Local Similarity 98.9%; Pred. KO 1e-16;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      7  GCTCCGCCCGCTGTCATGAGATGATGAAGAGGCTGCTGGGATTGACGTGAGGGG 66
Db      17  GCTCCGCCCGCTGTCATGAGATGATGAAGAGGCTGCTGGGATTGACGTGAGGGG 76

Oy      67  CAGGATGGCTATATTTCTGGAGGCA 93
Db      77  CAGGATGGCTATATTTCTGGAGGCA 103

Search completed: December 15, 2002. 01:28:14
Job time : 3319 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:17:53 : Search time 307 Seconds
(without alignments)
1335,061 Million cell updates/sec

Title: US-09-762-105-14

Perfect score: 182
Sequence: 1 gngctgctcccccgcgcgc.....tgactgtggacagctagc 182

Scoring Table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
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3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
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6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
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20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Prad. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	182	100.0	182	21	AZ61373		Nucleotide sequenc
2	182	100.0	1961	21	AZ61384		Nucleotide sequenc
3	182	100.0	5263	21	AZ61386		Nucleotide sequenc
4	164.4	90.3	182	21	AZ61374		Nucleotide sequenc
5	159.4	87.6	161	21	AZ61375		Nucleotide sequenc
6	111.2	61.1	168	22	AZ68175		Prrn/GiOL fusion n
7	111.2	61.1	168	22	AZ68175		Nucleotide sequenc
8	111.2	61.1	168	22	AZ65352		Nucleotide sequenc
9	93.6	51.4	191	21	AZ61361		Prrn/GiOL promoter

10	93.6	51.4	227	21	AZ61360		Nucleotide sequenc
11	93.6	51.4	227	21	AZ61362		Nucleotide sequenc
12	93.6	51.4	1049	22	AAF81268		DNA fragment desig
13	93.6	51.4	1985	21	AZ61382		Nucleotide sequenc
14	92.2	50.7	183	21	AZ61369		Nucleotide sequenc
15	92.2	50.7	185	21	AZ61372		Nucleotide sequenc
16	92.2	50.7	195	21	AZ61368		Nucleotide sequenc
17	90.0	49.5	131	22	AAF81259		Plastid rRNA
18	90.0	49.5	131	22	AAF81259		Plastid rRNA
19	90.0	49.5	154	21	AZ61364		Nucleotide sequenc
20	90.0	49.5	159	21	AZ61366		Nucleotide sequenc
21	90.0	49.5	195	21	AZ61365		Nucleotide sequenc
22	90.0	49.5	195	21	AZ61367		Nucleotide sequenc
23	90.0	49.5	196	21	AZ61363		Nucleotide sequenc
24	90.0	49.5	1953	21	AZ61381		Nucleotide sequenc
25	89.6	49.2	171	16	AAQ94853		Prrn/GiOL promoter
26	89.6	49.2	171	16	AAQ94853		Nucleotide sequenc
27	89.6	49.2	203	21	AZ61371		Regulatory region
28	86.4	47.3	129	20	AZ61340		Regulatory region
29	86.4	47.3	140	20	AZ61424		5' and 3' regulato
30	86.4	47.3	164	20	AZ61431		Regulatory region
31	85.8	47.1	127	22	AAF84276		Plastid 16S rRNA p
32	85.8	47.1	201	18	AAF66301		DNA of upstream re
33	85.8	47.1	6477	22	AAF67997		Chloroplast gene t
34	85.4	46.9	161	20	AZ61423		5' and 3' regulato
35	85.4	46.9	165	20	AZ61409		Prrn promoter sequ
36	85.4	46.9	184	20	AAF89143		Prrn/GiOL promoter
37	85.4	46.9	258	20	AZ61429		Regulatory region
38	85.4	46.9	258	20	AZ61429		Regulatory region
39	85.4	46.9	1134	18	AAF85195		Plastid targeting
40	85.4	46.9	1134	20	AZ61415		Selectable marker
41	85.4	46.9	1183	21	AZ61376		Nucleotide sequenc
42	85.4	46.9	1208	20	AZ61433		Regulatory region
43	85.4	46.9	1416	20	AZ61432		Regulatory region
44	85.4	46.9	1417	18	AAF85196		Plastid targeting
45	85.4	46.9	2962	20	AZ61408		Targeting region

ALIGNMENTS

RESULT 1	
AZ61373	
ID	AZ61373 standard; DNA; 182 BP.
XX	
XX	AZ61373:
XX	
DT	19-JUN-2000 (first entry)
XX	
DE	Nucleotide sequence of chimeric promoter PrrnLT7g10-DB/Ec.
DE	
XX	Chimeric promoter: plastid rRNA operon Omega-type promoter; haemoglobin;
KW	Prrn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
XX	
XX	Synthetic.
XX	
PH	Key
FT	promoter
FT	Location/Qualifiers
FT	7..89
FT	/*tag= a
FT	/note= "Prrn plastid promoter"
FT	141..144
FT	/*tag= b
FT	/note= "Shine-Dalgarno sequence"
XX	
XX	WO200007431-A1.
PD	
PD	17-FEB-2000.
XX	
PF	03-AUG-1999;
XX	99WO-US17806.
XX	
PR	03-AUG-1998;
XX	98US-0095163.
PR	03-AUG-1998;
XX	98US-0095167.
PR	15-DEC-1998;
XX	98US-0112257.

us-09-762-105-14.rng

[illegible]

heterologous protein in plastids (e.g. heterologous protein in the leader sequence and a downstream box element).

Disclosure: Fig 32: 16App: English.

The present sequence represents a DNA construct of the invention. The specification describes the DNA constructs for expressing heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter element, a leader sequence and a downstream box element operably linked to a coding region of the heterologous protein. The DNA molecule encoded by the region enhances translational efficiency of the heterologous protein. The DNA construct plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin or household enzymes. Plants which can be used with the constructs of the invention include wheat, barley, sorghum, sugar cane, rice, wheat, barley, oat, soy or turf grass.

Sequence 161 BP: 552 A: 430 C: 486 G: 493 T: 0 other:

	Query Match	Similarity	100.0%	Pred. NO.	2.9e-50:	Mismatches	Indels	Caps
	Matches	182:	Conservative	0:				
OY	1	GAGCTCGGTCGCCGGCCTGTGCATAGCAATCCATACAGAGCTTCTGGGATTGAACGCG	60					
OY	1							
OY	1							
OY	1							
DB	1	GAGCTCGGTCGCCGGCCTGTGCATAGCAATCCATACAGAGCTTCTGGGATTGAACGCG	60					
DB	1							
DB	1							
OY	61	AGSGGGCACGGATGGCTATATTTCTGGGAGGAGACACACACGGTTCCTCCACTAGANATA	120					
OY	61	AGSGGGCACGGATGGCTATATTTCTGGGAGGAGACACACACGGTTCCTCCACTAGANATA	120					
DB	61	AGSGGGCACGGATGGCTATATTTCTGGGAGGAGACACACACGGTTCCTCCACTAGANATA	120					
OY	121	ATTTTGTTTAACCTTAAGNAGGAGATATACATATGCGAAGCATGTGGACAGCTA	180					
OY	121							
OY	121							
DB	121	ATTTTGTTTAACCTTAAGNAGGAGATATACATATGCGAAGCATGTGGACAGCTA	180					
DB	121							
OY	181	GC 182						

[illegible]

The present sequence represents a chimeric plastid rRNA operon encoding a promoter with the T7 phage gene and Escherichia coli Shine-Dalgarno box. The chimeric promoter is used, as a expressing sequence, to produce recombinant DNA constructs in higher plants. The DNA sequence contains a regulatory region which includes a promoter construct containing sequence and a downstream box element operated by a coding region of the heterologous protein mRNA molecule encoded by the region enhances translational efficiency are used for producing transgene in the DNA construct. Plants having high levels of heterologous protein monoclonal antibodies or pharmaceuticals expression of protein production agronomic, industrial or pharmaceutical products haemoglobin, industrial or of vaccines, healthcare products which can be transformed with the constructs household enzymes include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.

Query Match 90.3%; Score 164.4; DB 21; Length 182;
Best Local Similarity 94.0%; Pred. No. 8.2e-45;
Matches 171; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 GAGCTGGTCCCGCCGTCATGAGATGGAAGCGTCGTGGATTGACGTG 60
Db 1 GAGCTGGTCCCGCCGTCGTTCATGAGATGGAAGCGTCGTGGATTGACGTG 60
Oy 61 AGCGGCGAGCGTGATATTTCTCGGAGGAGACCAACGGTTCCCACTAGAATA 120
Oy 61 AGCGGCGAGCGTAGCTATATTTCTCGGAGGAGACCAACGGTTCCCACTAGAATA 120
Oy 61 AGCGGCGAGCGTAGCTATATTTCTCGGAGGAGACCAACGGTTCCCACTAGAATA 120
Oy 131 ATTGTGTTACTGTAAGAGCATATACATATGCAGCATGCTGGTGACAGCCTA 180
Db 131 ATTGTGTTACTGTAAGAGCATATACATATGCAGCATGCTGGTGACAGCCTA 180
Oy 181 GC 182
Oy 181 GC 182

RESULT 5
AAZ61375 standard; DNA; 161 BP.
XX AAZ61375;
AC AAZ61375; (first entry)
XX 19-JUN-2000
XX Nucleotide sequence of chimeric promoter PrrnL7g10-DB.
DE Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
KW Firm promoter; protein expression; vaccine; enzyme; T7 phage gene 10; sb. 1.
XX Synthetic.
OS Synthetic.
XX Key Location/Qualifiers
FH Promoter 7..89
FT /*tag= a
FT /note= "Prrn plastid promoter"
FT misc_signal 14..141
FT /*tag= b
FT /note= "Shine-dalgarno sequence"
XX WO200007431-A1.
FN
XX
XX 17-FEB-2000.
XX
PF 03-AUG-1999; 99MO-US17806.
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
PR 03-AUG-1998;
PR 15-DEC-1998; 98US-0112257.
PR #
+

DR 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (ROTF) UNIV RUTGERS STATE NEW JERSEY.
XX Maliga P., Kuroda H., Khan MS:
XX WPT: 2000-205525/A8.
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plastids of higher plants, includes promoter, a
XX leader sequence and a downstream box element -
XX Claim 4; Fig 3D; 164pp; English.
XX The present sequence represents a chimeric plastid rna operon
XX omega-type (prn) promoter with a leader gene and a synthetic
XX downstream box. These recombinant DNA constructs for expressing
XX sequences encode various proteins in the plastids of higher plants as a promoter
XX construct comprise a 5' regulatory region "box element operably linked
XX element, a leader sequence and a downstream box element. The chimeric regulatory
XX construct is used for increasing the translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transgenic plant
XX monocot and dicot plants having high level expression of heterologous protein
XX expression. They can be used in pharmaceutical expression of proteins with
XX agronomics, healthcare products like human hemoglobin, and other
XX household enzymes. Plants which can be transformed include maize, millet, sorghum, sugar cane, rice,
XX of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.

XX Sequence 161 BP; A3 A4 30 C; 48 G; 40 T; 0 other:
XX Query Match: 97.6%; Score 159.4; DB 21; Length 161;
XX Best Local Similarity: 99.4%
XX Matches: 160; Conservativity: 0; Mismatches: 1; Indels: 0; Gaps: 0;

OY 1 GAGCTCGCTCCGCCGCCTGGTTCATAGCAATGAGAGCGGTGGAGATTGACGTCG 60
DB 1 GAGCTCGCTCCGCCGCCTGGTTCATAGCAATGAGAGCGGTGGAGATTGACGTCG 50
OY 61 AGCGGCGAGGAGTGCTATTTCGCGAGGACGACGACGAGCGTTCCCACTAGAATA 120
DB 61 AGCGGCGAGGAGTGCTATTTCGCGAGGACGACGACGAGCGTTCCCACTAGAATA 120
OY 121 ATTTTGTAACTTCTTAAGAGGAGATATACATATGCGAACC 161
DB 121 ATTTTGTAACTTCTTAAGAGGAGATATACATATGCGTASC 161

RESULT 6
ANZ88175
ID AAZ88175 standard; DNA; 168 BP.
XX ANZ88175:
XX
XX 25-APR-2000 (first entry)
XX Prn/G10L fusion nucleic acid sequence.
DE Tobacco; ribosome binding site; aptrotrin; herbicide tolerance; plastid;
KW human growth hormone; insulin; ds.
XX Nicotiana sp.
OS Synthetic.
XX WO200003022-A2.
PN 20-JAN-2000.
XX 10-JUL-1999; 99WO-US15472.
PF

```

XX PR 10-JUL-1998; 98US-0113257.
XX PA (CALJ ) CALGENE LLC.
XX PI Hajdukiewicz P, McBride KB, Nehra N, Schaaf DJ, Stalker DM;
XX PI Staub JM, Ye G;
XX DR WPI; 2000-147617/13.
XX
XX New construct useful for producing herbicide tolerance in plants and
XX for directing production of pharmaceutical proteins -
XX
XX Example 1; Fig 6; 62pp: English.
XX
XX The present invention describes a construct (I) comprising a plant
XX plasmid promoter region, a DNA sequence capable of conferring herbicide
XX tolerance in the plant cell and a transcription termination region
XX operably joined in the 5'-3' direction. (I) is useful for producing
XX herbicide tolerance in a plant cell, comprising transforming plasmids of
XX the plant cell with (I) and the herbicide tolerance is useful for
XX selecting cells transformed with (I) from non-transformed cells. Plasmid
XX expression construct is useful for directing expression of DNA sequences
XX encoding enzymes involved in herbicide tolerance or for producing
XX pharmaceutical proteins in plant cells. (I) is useful for producing
XX insulin precursors. Transplastomic plants have high level of tolerance to
XX herbicides. Protein levels obtained from plasmid expression constructs
XX is found to be higher than from nuclear expression constructs. Plasmid
XX expression constructs utilising 16S ribosomal RNA operon (Prn)/G10L
XX promoter/RBS sequence accumulates 50-3500 fold higher levels of protein
XX than nuclear expression constructs. By including targeting sequences,
XX the expressed proteins can be targeted to particular suborganelar
XX regions for e.g. thylakoid membrane, which facilitates increased
XX stability and proper protein folding. Insect or disease
XX resistance can be achieved by expressing a Prn/G10L fusion nucleic
XX acid sequence. The present sequence represents a Prn/G10L fusion nucleic
XX acid sequence, which is used in an example from the present invention
XX for the production of expression constructs.
XX
XX Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
XX
XX Query Watch 61.1%; Score 111.2; DB 21; Length 168;
XX Best Local Similarity 88.7%; Pred. No. 3.8e-27;
XX Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;
XX
XX QY 7 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTGACGTAGGGGG 66
XX Db 23 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTGACGTAGGGGG 66
XX
XX QY 67 CAGGATGCGCTATATTTCTGGAGGAGACACACCGTTTCCCTAGTAATAATTTTG 126
XX Db 23 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTGACGTAGGGGG 82
XX
XX QY 83 CAGGATGCGCTATATTTCTGGAGGAGCA-----ACTCCGGCGAATTGTAGAAATATTTTG 138
XX Db 83 CAGGATGCGCTATATTTCTGGAGGAGCA-----ACTCCGGCGAATTGTAGAAATATTTTG 138
XX
XX QY 127 TTTAACTTTAAGAAGGAGATATACATATGG 156
XX Db 139 TTTAACTTTAAGAAGGAGATATACCATGG 168
XX
XX RESULT 8
XX ID AAF57902 standard; DNA; 168 BP.
XX AC AAF57902;
XX
XX DT 18-APR-2001 (first entry)
XX XX Prn/G10L promoter/RBS hybrid coding sequence.
XX XX Green fluorescent protein; GFP; translational fusion; gene expression;
XX KW herbicide tolerance; pharmaceutical protein; disease resistance; ds.
XX OS Synthetic.
XX
XX PN WO200104331-A2.
XX XX 18-JAN-2001.
XX XX 10-JUL-2000; 2000WO-US18727.
XX XX 10-JUL-1999; 99US-0351123.
XX XX (CALJ ) CALGENE LLC.
XX
XX PI Hajdukiewicz P;
XX DR WPI; 2001-138356/14.
XX
XX Novel constructs for expressing herbicide tolerance genes in plant cell
XX plasmids, comprises a promoter functional in plant plasmid, a DNA
XX sequence conferring herbicide tolerance and transcription terminator -
XX
XX Example 1; Fig 6; 70pp: English.
XX
XX The specification describes a construct comprising a promoter functional
XX in a plant plasmid, a DNA sequence capable of conferring tolerance in a
XX plant cell to at least one herbicide compound when the DNA sequence
XX is transcribed in plant cell plasmids, and a transcription termination
XX region, in the 5'-3' direction of transcription. The construct is useful
XX for producing a herbicide tolerant plant cell. The construct is
XX also useful for producing a herbicide tolerant plant cell. The construct is
XX eukaryotic and prokaryotic, in plant plasmids. It is useful for genetic
XX engineering of plant cells, and which provide for enhanced expression of
XX EPSPS proteins or hGH protein in plant cell plasmids. The present
XX sequence represents a hybrid comprising plasmid 16S ribosomal RNA
XX operon, and a synthetic G10L ribosome binding site (RBS). The hybrid
XX is used to produce constructs of the invention.
XX
XX Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
XX
XX Query Watch 61.1%; Score 111.2; DB 22; Length 168;
XX Best Local Similarity 88.7%; Pred. No. 3.8e-27;
XX Matches 133; Conservative 0; Mismatches 13; Indels 4; Gaps 1;
XX
XX QY 7 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTGACGTAGGGGG 66
XX Db 23 GCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTGCTGGGATTGACGTAGGGGG 82
XX
XX QY 67 CAGGATGCGCTATATTTCTGGAGGAGACACACCGTTTCCCTAGTAATAATTTTG 126
XX Db 83 CAGGATGCGCTATATTTCTGGAGGAGCA-----ACTCCGGCGAATTGTAGAAATATTTTG 138
XX
XX QY 127 TTTAACTTTAAGAAGGAGATATACATATGG 156
XX Db 139 TTTAACTTTAAGAAGGAGATATACCATGG 168
XX
XX RESULT 8
XX ID AAF57902 standard; DNA; 168 BP.
XX AC AAF57902;
XX
XX DT 18-APR-2001 (first entry)
XX XX Prn/G10L promoter/RBS hybrid coding sequence.
XX XX Green fluorescent protein; GFP; translational fusion; gene expression;
XX KW herbicide tolerance; pharmaceutical protein; disease resistance; ds.
XX OS Synthetic.
XX
XX PN WO200104331-A2.
XX XX 18-JAN-2001.
XX XX 26-JUN-2000; 2000WO-US18096.

```

[illegible]

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XX /*note= "Shine-Dalgarno sequence"
FN W0200007431-AL.
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 99US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Kuroda H, Khan MS;
XX WPI: 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plasmids of higher plants, includes promoter, a
XX leader sequence and a downstream box element -
XX
XX Claim 3; Fig 3A; 164pp: English.
XX
XX The present sequence represents a chimeric plasmid RNA operon
XX omega-type (Prn) promoter with atpB translation control sequences and
XX a wild type downstream box. The chimeric promoter is used, as a 5',
XX regulatory sequence, to produce recombinant DNA constructs for expressing
XX heterologous proteins in the plasmids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element operably linked
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
XX expression. They can be used to drive expression of proteins with
XX agronomic, industrial or pharmaceutical importance, including production
XX of vaccines, healthcare products like human haemoglobin, industrial or
XX household enzymes. Plants which can be transformed with the constructs
XX of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
XX
XX Sequence 227 BP; 58 A; 42 G; 55 G; 72 T; 0 other:
XX
XX Query Match 51.4%; Score 93.6; DB 21; Length 227;
XX Best Local Similarity 75.0%; Pred. No. 3e-21;
XX Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
XX
XX 1 GAGCTGCTCCCTCCCGCCGCTGCTCAATGAGATGGATAGACGCTCTCGGGATTGACGTG 60
XX |
XX 1 GAGCTGCTCCCTCCCGCCGCTGCTCAATGAGATGGATAGACGCTCTCGGGATTGACGTG 60
XX |
XX 61 AGGGGCGAGGATGGCTATATTTCTGGAGGAGACCAACAGCGTTTCCCACTAGAAATA 120
XX |
XX 61 AGGGGCGAGGATGGCTATATTTCTGGAGGAGATTAACCGATGACGCTGCAACGCGACAT 120
XX |
XX 121 TATTTTAATTCGATTAATTTTGCAGAAATTTTCG 156
XX |
XX
XX RESULT 11
XX AAZ61362
XX ID AAZ61362 standard; DNA: 227 BP.
XX AC AAZ61362;
XX AA
XX 19-JUN-2000 (first entry)
XX

```

Nucleotide sequence of chimeric promoter PrnLatp8+Dm8.

Chimeric promoter; plasmid RNA operon omega-type promoter; haemoglobin; Prn promoter; atpB; protein expression; vaccine; enzyme; ss.

Synthetic.

Key

Location/Qualifiers

789

/*tag= a

/*note= "Prn plasmid promoter"

114..116

/*tag= b

/*note= "Shine-Dalgarno sequence"

W0200007431-AL.

17-FEB-2000.

03-AUG-1999; 99WO-US17806.

03-AUG-1998; 98US-0095163.

03-AUG-1998; 98US-0095167.

15-DEC-1998; 98US-0112257.

29-APR-1999; 99US-0131611.

11-JUN-1999; 99US-0138764.

(RUF) UNIV RUTGERS STATE NEW JERSEY.

Maliga P, Kuroda H, Khan MS;

WPI: 2000-205525/18.

New recombinant DNA constructs, for expressing high levels of heterologous protein in plasmids of higher plants, includes promoter, a leader sequence and a downstream box element -

Claim 3; Fig 3A; 164pp: English.

The present sequence represents a chimeric plasmid RNA operon omega-type (Prn) promoter with atpB translation control sequences and a mutated downstream box. The chimeric promoter is used, as a 5' regulatory sequence, to produce recombinant DNA constructs for expressing heterologous proteins in the plasmids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter element, a leader sequence and a downstream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing transformed monocot and dicot plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.

Sequence 227 BP; 64 A; 40 G; 59 G; 64 T; 0 other:

Query Match 51.4%; Score 93.6; DB 21; Length 227; Best Local Similarity 75.0%; Pred. No. 3e-21; Matches 117; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

1 GAGCTGCTCCCTCCCGCCGCTGCTCAATGAGATGGATAGACGCTCTCGGGATTGACGTG 60

1 GAGCTGCTCCCTCCCGCCGCTGCTCAATGAGATGGATAGACGCTCTCGGGATTGACGTG 60

61 AGGGGCGAGGATGGCTATATTTCTGGAGGAGACCAACAGCGTTTCCCACTAGAAATA 120

61 AGGGGCGAGGATGGCTATATTTCTGGAGGAGATTAACCGATGACGCTGCAACGCGACAT 120

121 ATTTTGTACTTTTAAAGAGGATATACATATGG 156

121 ATTTTGTACTTTTAAAGAGGATATACATATGG 156

AAZ61362

AAZ61362 standard; DNA: 227 BP.

AAZ61362;

19-JUN-2000 (first entry)

```

Db 121 TATTTTAAATTCGATTAATTTTTCGAAAACATTTCG 156
RESULT 12
AA#81268
ID AAF81268 standard: DNA: 1049 BP.
AC AAF81268;
XX 05-JUN-2001 (first entry)
XX DNA fragment designed for CRE-induced expression of recombinant protein.
XX GRP recombinase; plasmid genome manipulation;
XX Site specific recombination; ds.
XX Synthetic.
XX WO200121768-A1.
XX WO200121768-A1.
PD 21-SEP-2000; 2000WO-US25930.
XX 21-SEP-1999; 99US-0155007.
PR 13-JUN-2000; 2000US-0211139.
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX PA Maliga P, Cornielle S, Lutz K;
XX WPI: 2001-266071/27.
XX Removing target nucleic acid sequences e.g. selectable marker genes.
XX genes involved in plant cell metabolism, growth development and
XX fertility from plastid genomes, by Cre-mediated site specific
XX recombination -
XX Example 3; Page 48; 83pp; English.
XX The present sequence was used in an example illustrating an invention
XX relating to a method for manipulating the genome of higher plants. The
XX method involves selecting a target nucleic acid encoding a marker excision sites
XX and plastid targeting sequence for homologous recombination into a
XX plastid genome at a target sequence. The method is useful for removing
XX heterologous sequences from the plastid genome, such as selectable
XX marker genes, and for introducing exogenous genes associated with male sterility, clipp
XX ribosomal proteins and ribosomal RNA operon sequences from the plastid
XX genome.
XX Sequence 1049 BP; 269 A; 235 C; 282 G; 263 T; 0 other;
Query Match 51.4%; Score 93.6; DB 22; Length 1049;
Best Local Similarity 75.0%; Pred. No. 5.4e-21;
Matches 107; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
OY 1 GAGCTCGTCGCCCGCGCTTCAATGAGATGATAGAGCTCGTGGGATTGACGTG 60
DB 1 GAGCTCGTCGCCCGCGCGCTTCAATGAGATGATAGAGCTCGTGGGATTGACGTG 60
OY 61 AGGGGCGAGGAGTGCCTATATTTCTGGGGGAGACACACAGCTTCCCTCAGAAATA 120
DB 61 AGGGGCGAGGAGTGCCTATATTTCTGGGGGAGATTAACCGATCGAGTCGACGCGATAT 120
OY 121 ATTTCTTTAACTTTAAGAGGAGATATACATATGCG 156
DB 121 TATTTTAAATTCGATTAATTTTTCGAAAACATTTCG 156
RESULT 13
AA#61382
AAZ61382 standard: DNA: 1985 BP.
XX AAZ61382;
XX 19-JUN-2000 (first entry)
XX Nucleotide sequence of DNA construct FLARE16-S2.
XX Green fluorescent protein; GFP; aadA; aptB; protein expression; vaccine;
XX haemoglobin; enzyme; psbA; ss.
XX Synthetic.
XX WO200007431-A1.
XX WO200007431-A1.
XX Key Location/Qualifiers
XX misc_feature /:221 a
XX misc_feature /note="stpB downstream box"
XX misc_feature 228..1010
XX misc_feature /tag= b
XX misc_feature 1056..1779
XX misc_feature /tag= c
XX misc_feature /note="green fluorescent protein region"
XX misc_feature 1790..1978
XX misc_feature /tag= d
XX misc_feature /note="psbA region"
XX WO200007431-A1.
XX 17-FEB-2000.
XX 99WO-US17806.
XX 03-AUG-1999; 99US-0095163.
XX 03-AUG-1998; 98US-012257.
XX 15-DEC-1998; 98US-013161.
XX 29-APR-1999; 99US-013161.
XX 11-JUN-1999; 99US-0138764.
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX Maliga P, Kuroda H, Khan MS;
XX WPI: 2000-205525/18.
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plastids of higher plants, includes promoter, a
XX leader sequence and a downstream box element -
XX Disclosure: Fig 30; 164pp; English.
XX The present sequence represents a DNA construct of the invention.
XX The specification describes recombinant DNA constructs for expressing
XX heterologous proteins in plastids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element operably linked
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of the heterologous protein
XX monoot and dicot plants having high levels of heterologous protein
XX expression. They can be used to drive expression of proteins with
XX agronomic, industrial or pharmaceutical importance, including production
XX of vaccines, healthcare products, and pharmaceuticals. The DNA
XX constructs of the invention include maize, millet, sorghum, sugar cane, rice,
XX wheat, barley, oat, rye or turf grass.
XX Sequence 1985 BP; 553 A; 431 C; 482 G; 519 T; 0 other;
Query Match 51.4%; Score 93.6; DB 21; Length 1985;
Best Local Similarity 75.0%; Pred. No. 6.9e-21;

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Matches 117: Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 GAGTCGCTCCCGCCGCGTTCATAGAGATGGAAGAGCGTCGTCGGGATTGACGTG 60
    |||||
Dy 1 GAGTCGCTCCCGCCGCGTTCATAGAGATGGAAGAGCGTCGTCGGGATTGACGTG 60
    |||||
QY 61 AGCGGCGAGGAGTGCCTATATTTCTGCGAGGAGGACACAGCGTTCCGACTAGAAATA 120
    |||||
Dy 61 AGCGGCGAGGAGTGCCTATATTTCTGCGAGGAGTAAACGATCGAGTCGACGCGACATT 120
    |||||
QY 121 ATTTTGTCTTAACATTTTAAAGAGCAGATATACATATGG 156
    |||||
Dy 121 TATTTTAAATTCGATAATTTTTCGAAAACATTTCCG 156
    |||||

RESULT 14
AAZ61369
ID AAZ61369 standard; DNA: 153 BP.
AC AAZ61369;
XX
XX
XX 19-JUN-2000 (first entry)
XX
DE Nucleotide sequence of chimeric promoter PrnlpSbB-DB.
XX
KW Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
KW Prn promoter; psbA; protein expression; vaccine; enzyme; ss.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH promoter 7..89
FT /*tag= a
FT /*note= "Prn plastid promoter"
FT misc_signal 148..149
FT /*tag= b
FT /*note= "Shine-Dalgarno sequence"
PN W0200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 98US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Kuroda H, Khan MS;
XX WPI: 2000-205525/18.
XX
XX The present sequence represents a chimeric plastid rRNA operon
XX omega-type (Prn) promoter with psbA translation control sequences,
XX without a downstream box element, and a downstream box element -
XX regulatory sequence to produce recombinant DNA constructs for expressing
XX heterologous proteins in the plastids of higher plants. The DNA
XX constructs comprise a 5' regulatory region which includes a promoter
XX element, a leader sequence and a downstream box element operably linked
XX to a coding region of the heterologous protein. The chimeric regulatory
XX region enhances translational efficiency of an mRNA molecule encoded by
XX the DNA construct. The DNA constructs are used for producing transformed
XX monocot and dicot plants having high levels of heterologous protein
```

```
CC expression. They can be used to drive expression of proteins with
CC agronomic, industrial or pharmaceutical importance, including production
CC of vaccines, healthcare products like human haemoglobin, industrial or
CC household enzymes. Plants which can be transformed with the constructs
CC of the invention include maize, millet, sorghum, sugar cane, rice,
CC wheat, barley, oat, rye or turf grass.
XX
SQ Sequence 153 BP: 36 A; 27 C; 47 G; 43 T; 0 other;
    50.7%; Score 92.2; DB 21; Length 153;
    Best Local Similarity 92.4%; Pred. No. 7.6e-21;
    Matches 97; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 GAGTCGCTCCCGCCGCGTTCATAGAGATGGAAGAGCGTCGTCGGGATTGACGTG 60
    |||||
Dy 1 GAGTCGCTCCCGCCGCGTTCATAGAGATGGAAGAGCGTCGTCGGGATTGACGTG 60
    |||||
QY 61 AGCGGCGAGGAGTGCCTATATTTCTGCGAGGAGGACACAGCGTTCCGACTAGAAATA 105
    |||||
Dy 61 AGCGGCGAGGAGTGCCTATATTTCTGCGAGGAGTAAACGATCGAGTCGACGCGATT 105
    |||||

RESULT 15
AAZ61372
ID AAZ61372 standard; DNA: 185 BP.
XX
XX AAZ61372;
XX
XX 19-JUN-2000 (first entry)
XX
XX Nucleotide sequence of chimeric promoter PrnlpSbA-DB(+GC).
XX
XX Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
XX Prn promoter; psbA; protein expression; vaccine; enzyme; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH promoter 7..89
FT /*tag= a
FT /*note= "Prn plastid promoter"
FT misc_signal 141..144
FT /*tag= b
FT /*note= "Shine-Dalgarno sequence"
PN W0200007431-A1.
XX
XX 17-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17806.
XX
XX 03-AUG-1998; 98US-0095163.
XX 03-AUG-1998; 98US-0095167.
XX 15-DEC-1998; 98US-0112257.
XX 29-APR-1999; 98US-0131611.
XX 11-JUN-1999; 99US-0138764.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Maliga P, Kuroda H, Khan MS;
XX WPI: 2000-205525/18.
XX
XX New recombinant DNA constructs, for expressing high levels of
XX heterologous protein in plastids of higher plants, includes promoter, a
XX leader sequence and a downstream box element -
XX Claim 3; Fig 3C; 164pp; English.
XX
XX The present sequence represents a chimeric plastid rRNA operon
XX omega-type (Prn) promoter with psbA translation control sequences,
XX without a downstream box. The chimeric promoter is used, as a 5'
XX regulatory sequence, to produce recombinant DNA constructs for expressing
XX
```

heterologous proteins in the plastids of higher plants. The DNA constructs comprising 5' and 3' untranslated regions which includes a promoter to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule. The DNA construct is used to transform plant cells producing heterologous protein monoco and then can be used to drive expression of heterologous protein of vaccines, healthcare products like human insulin, human growth hormone, industrial or pharmaceutical importance, including production of household enzymes in plants which are transformed with the constructs of the heterologous protein. The plants transformed with the constructs of the heterologous protein are wheat, maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.

Sequence 185 BP; 47 A; 35 C; 51 G; 52 T; 0 other;

Query Match 50.7%; Score 92.2; DB 21; Length 185;
Best Local Similarity 88.5%; Pred. No. 8.le-21;
Matches 100; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 GAGCTGCTCCCGCCGCTGTTCAATGAGATGCGTAAGAGCGCTCTGGGATTCACGTG 60
DB 1 GAGCTGCTCCCGCCGCTGTTCAATGAGATGCGTAAGAGCGCTCTGGGATTCACGTG 60

OY 61 AGGGGACAGGAGTGGCTATATTTCTGGGAGCAAAAAGCGCTTCATTCTCTATT 113
DB 61 AGGGGACAGGATGCTATATTTCTGGGAGCAAAAAGCGCTTCATTCTCTATT 113

Search completed: December 15, 2002, 00:32:45
Job time : 311 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:26:03 : Search time 67 Seconds
(without alignments)
833.062 Million cell updates/sec

Title: US-09-762-105-14
Perfect score: 182
Sequence: 1 gagctgcctcccccgcgcgc.....tgactgtggacagctcagc 182

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCFUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match %	Length	DB	ID	Description
C	1	89.6	49.2	171	1	US-08-217-360-16	Sequence 16, Appl
	2	86.4	47.5	129	2	US-08-189-256A-25	Sequence 25, Appl
	3	86.4	47.5	129	4	US-09-193-853-25	Sequence 25, Appl
	4	86	47.3	140	2	US-08-189-256A-19	Sequence 19, Appl
	5	86	47.3	140	4	US-09-193-853-19	Sequence 19, Appl
	6	86	47.3	164	2	US-08-189-256A-26	Sequence 26, Appl
	7	86	47.3	164	4	US-09-193-853-26	Sequence 26, Appl
	8	85.4	46.9	161	2	US-08-189-256A-18	Sequence 18, Appl
	9	85.4	46.9	161	4	US-09-193-853-18	Sequence 18, Appl
	10	85.4	46.9	165	2	US-08-189-256A-4	Sequence 4, Appl
	11	85.4	46.9	165	4	US-09-193-853-4	Sequence 4, Appl
	12	85.4	46.9	168	2	US-08-189-256A-2	Sequence 2, Appl
	13	85.4	46.9	168	4	US-09-193-853-2	Sequence 2, Appl
	14	85.4	46.9	184	4	US-09-283-419-3	Sequence 3, Appl
	15	85.4	46.9	258	2	US-08-189-256A-24	Sequence 24, Appl
	16	85.4	46.9	258	4	US-09-193-853-24	Sequence 24, Appl
	17	85.4	46.9	300	4	US-09-202-316-4	Sequence 4, Appl
	18	85.4	46.9	300	4	US-09-202-316-7	Sequence 7, Appl
	19	85.4	46.9	1134	2	US-08-189-256A-10	Sequence 10, Appl
	20	85.4	46.9	1134	4	US-09-193-853-10	Sequence 10, Appl
	21	85.4	46.9	1143	4	US-09-142-114B-6	Sequence 6, Appl
	22	85.4	46.9	1208	2	US-08-189-256A-28	Sequence 28, Appl
	23	85.4	46.9	1208	4	US-09-193-853-28	Sequence 28, Appl
	24	85.4	46.9	1416	2	US-08-189-256A-27	Sequence 27, Appl
	25	85.4	46.9	1416	4	US-09-193-853-27	Sequence 27, Appl
	26	85.4	46.9	1417	4	US-09-142-114B-7	Sequence 7, Appl
	27	85.4	46.9	2962	2	US-08-189-256A-3	Sequence 3, Appl

c 28 85.4 46.9 2962 4 US-09-193-853-3 Sequence 3, Appl
29 84.8 46.6 3984 1 US-08-040-753-1 Sequence 1, Appl
30 83.8 46.0 105 4 US-09-597-877-9 Sequence 9, Appl
31 83.2 45.7 187 1 US-08-096-182A-7 Sequence 7, Appl
32 83.2 45.7 187 1 US-08-877-109-7 Sequence 7, Appl
33 83.2 45.7 187 3 US-08-798-760-7 Sequence 7, Appl
34 83.2 45.7 187 5 PCT-US94-08327-7 Sequence 7, Appl
35 83.2 45.7 187 1 US-08-217-360-17 Sequence 17, Appl
36 83 45.6 166 1 US-08-217-360-17 Sequence 17, Appl
37 82.8 45.5 104 2 US-09-337-028-9 Sequence 9, Appl
38 82.8 45.5 104 4 US-08-189-256A-1 Sequence 1, Appl
39 82.2 45.2 150 2 US-08-193-853-1 Sequence 1, Appl
40 82.2 45.2 150 4 US-08-902-623-44 Sequence 44, Appl
c 41 72.2 39.7 146 2 US-08-929-967-5 Sequence 5, Appl
42 71 39.0 4411 2 US-08-929-967-5 Sequence 5, Appl
43 71 39.0 5443 2 US-08-929-967-5 Sequence 5, Appl
44 71 39.0 5443 2 US-08-929-967-5 Sequence 5, Appl
45 70.8 38.9 369 4 US-09-265-919-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-217-360-16
; Sequence 16 Application US/08217360
; PCT/US94-08327-7
; GENERAL INFORMATION:
; APPLICANT: MALIGA, Pal
; TITLE OF INVENTION: METHODS FOR PRODUCING CYTOPLASMIC
; TITLE OF INVENTION: MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF H
; NUMBER OF SEQUENCES: 17
; TITLE OF INVENTION: SEED
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Damm, Dorfman, Herrell and Skillman,
; STREET: 601 N. Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; WARNING: This release is 1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/217,360
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers University
; TELEPHONIC COMMUNICATION:
; TELEPHONE: (215)563-4100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: HUMAN
; ANTI-SENSE: NO
US-08-217-360-16

Query Match 49.2% Score 89.6; DB 1; Length 171;
Best Local Similarity 78.3%; Pred. No. 1.3e-21;
Matches 130; Conservative 0; Mismatches 14; Indels 22; Gaps 1;
oy 7 GCTCCCCCGCGTCGTCATGAGATGAGAGCTCGTGGATTCAGTCGAGGGG 66

Db 6 GCTCCCCCGCGTCTTCATAGAGATGGATAGAGGCTCTGGGATTGACGTGAGCGGG 65

Qy 67 CAGGGATGGCTATATTTCTTGGGAGGAGCACCACGAGGTTTCCC 110

Db 66 CAGGGATGGCTATATTTCTTGGGAGGAGCACCACGAGGTTTCCC 109

RESULT 3

US-08-189-256A-25 Application US/08189256A

Patent No. 5677402

GENERAL INFORMATION:

APPLICANT: Mallgro, Pal

APPLICANT: Staub, Jeffrey V.

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Kanevski, Ivan

APPLICANT: Carrier, Helaine

TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plasmids of Multicellular Plants and

TITLE OF INVENTION: Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM: disk

MODEM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/189,256A

PRIOR APPLICATION NUMBER: US/08/189,256A

FILING DATE: 31-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA: US 08/111,398

APPLY DATE: 25-AUG-1993

PRIOR APPLICATION DATA: US 07/518,763

APPLICATION NUMBER: 90

FILING DATE: INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELEPHONE: (215) 563-4044

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 base pairs

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANNT-SENSE: NO

US-08-189-256A-25

Query Match 47.5% Score 86.4; DB 2; Length 129;

Best Local Similarity 89.4%; Pred. No. 1.5e-20;

Mismatches 11; Indels 0; Caps 0;

Matches 93; Conservative 0;

Qy 7 GCTCCCCCGCGTCTTCATAGAGATGGATAGAGGCTCTGGGATTGACGTGAGCGGG 66

Db 6 CAGGGATGGCTATATTTCTTGGGAGGAGCACCACGAGGTTTCCC 110

Qy 67 CAGGGATGGCTATATTTCTTGGGAGGAGCACCACGAGGTTTCCC 109

Db 66 CAGGGATGGCTATATTTCTTGGGAGGAGCACCACGAGGTTTCCC 109

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: Patent No. 6388168
: GENERAL INFORMATION:
: APPLICANT: Maligna, Pal
: APPLICANT: Svab, Zora
: APPLICANT: Staub, Jeffrey
: APPLICANT: Zoubenko, Oleg V.
: APPLICANT: Allison, Lori A.
: APPLICANT: Carrier, Helaine
: APPLICANT: Kanevski, Ivan
: TITLE OF INVENTION: DNA Constructs and Methods for Stably
: Transforming Plasmids of Multicellular Plants and
: Expressing Recombinant Proteins Therein
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dann, Dorfman, Herrell and Skillman
: STREET: 1601 Market Street Suite 720
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103-2307
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/193,853
: FILING DATE: 31-JAN-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/189,256
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/518,763
: FILING DATE: 01-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Janet E.
: REGISTRATION NUMBER: 36,252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-4100
: TELEFAX: (215) 563-4100
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-09-193-853-19

Query Match 47.3%; Score 86; DB 2; Length 140;
Best Local Similarity 90.2%; Pred. No. 2.1e-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 7 GCTCCCCCGCGCTTCATAGAGAGCTCGTGGGATTCGACGTGAGGGG 66
Db 17 GCTCCCCCGCGCTTCATAGAGAGCTCGTGGGATTCGACGTGAGGGG 76

QY 67 CAGGGATGCTATATTCTTGGGAGGAGACCAACACGGTTTC 108
Db 77 CAGGGATGCTATATTCTTGGGAGGAGACCAACACGGTTTC 118

RESULT 5
: Sequence 19, Application US/09193853
: GENERAL INFORMATION:
: APPLICANT: Maligna, Pal
: APPLICANT: Svab, Zora
: APPLICANT: Staub, Jeffrey
: APPLICANT: Zoubenko, Oleg V.
: APPLICANT: Allison, Lori A.
: APPLICANT: Carrier, Helaine
: APPLICANT: Kanevski, Ivan
: TITLE OF INVENTION: DNA Constructs and Methods for Stably
: Transforming Plasmids of Multicellular Plants and
: Expressing Recombinant Proteins Therein
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dann, Dorfman, Herrell and Skillman
: STREET: 1601 Market Street Suite 720
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103-2307
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/189,256A
: FILING DATE: 31-JAN-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/111,398
: FILING DATE: 25-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/518,763
: FILING DATE: 01-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Janet E.
: REGISTRATION NUMBER: 36,252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-4100
: TELEFAX: (215) 563-4100
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-08-189-256A-19

Query Match 47.3%; Score 86; DB 2; Length 140;
Best Local Similarity 90.2%; Pred. No. 2.1e-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 7 GCTCCCCCGCGCTTCATAGAGAGCTCGTGGGATTCGACGTGAGGGG 66
Db 17 GCTCCCCCGCGCTTCATAGAGAGCTCGTGGGATTCGACGTGAGGGG 76

QY 67 CAGGGATGCTATATTCTTGGGAGGAGACCAACACGGTTTC 108
Db 77 CAGGGATGCTATATTCTTGGGAGGAGACCAACACGGTTTC 118

RESULT 6
: Sequence 26, Application US/08189256A
: GENERAL INFORMATION:
: APPLICANT: Maligna, Pal
: APPLICANT: Svab, Zora
: APPLICANT: Staub, Jeffrey
: APPLICANT: Zoubenko, Oleg V.
: APPLICANT: Allison, Lori A.
: APPLICANT: Carrier, Helaine
: APPLICANT: Kanevski, Ivan
: TITLE OF INVENTION: DNA Constructs and Methods for Stably
: Transforming Plasmids of Multicellular Plants and
: Expressing Recombinant Proteins Therein
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dann, Dorfman, Herrell and Skillman
: STREET: 1601 Market Street Suite 720
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103-2307
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/193,853
: FILING DATE: 31-JAN-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/189,256
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/518,763
: FILING DATE: 01-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Janet E.
: REGISTRATION NUMBER: 36,252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-4100
: TELEFAX: (215) 563-4100
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-09-193-853-19

Query Match 47.3%; Score 86; DB 4; Length 140;
Best Local Similarity 90.2%; Pred. No. 2.1e-20;
Matches 92; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 7 GCTCCCCCGCGCTTCATAGAGAGCTCGTGGGATTCGACGTGAGGGG 66
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QY 67 CAGGGATGCTATATTCTTGGGAGGAGACCAACACGGTTTC 108
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RESULT 6
: Sequence 26, Application US/08189256A
: GENERAL INFORMATION:
: APPLICANT: Maligna, Pal
: APPLICANT: Svab, Zora
: APPLICANT: Staub, Jeffrey
: APPLICANT: Zoubenko, Oleg V.
: APPLICANT: Allison, Lori A.
: APPLICANT: Carrier, Helaine
: APPLICANT: Kanevski, Ivan
: TITLE OF INVENTION: DNA Constructs and Methods for Stably
: Transforming Plasmids of Multicellular Plants and
: Expressing Recombinant Proteins Therein
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dann, Dorfman, Herrell and Skillman
: STREET: 1601 Market Street Suite 720
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103-2307
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/193,853
: FILING DATE: 31-JAN-1994
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/189,256
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/518,763
: FILING DATE: 01-MAY-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Janet E.
: REGISTRATION NUMBER: 36,252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-4100
: TELEFAX: (215) 563-4100
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 140 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-09-193-853-19
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STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189/256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
FILING DATE: 01-MAY-1990
PRIOR APPLICATION NUMBER: US 07/518,763
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-18

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Best Local Similarity 98.9%; Pred. No. 3.5e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 67 CAGGATGCGCTATATTCTTGGAGGGA 93
Db 83 CAGGATGCGCTATATTCTTGGAGGGA 109
RESULT 9
US-09-193-853-18
Sequence 18, Application US/09193853
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Malliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for stably
transforming plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dana, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193/853
FILING DATE: 01-MAY-1990
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-193-853-18

Query Match 46.9%; Score 85.4; DB 4; Length 161;
Best Local Similarity 98.9%; Pred. No. 3.5e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCCGCGCGCTCAATGAGTGAAGAGCGCTGCGGATTGACGTGAGGGGG 66
Db 23 GCTCCCGCGCGCTCAATGAGTGAAGAGCGCTGCGGATTGACGTGAGGGGG 82
QY 67 CAGGATGCGCTATATTCTTGGAGGGA 93
Db 83 CAGGATGCGCTATATTCTTGGAGGGA 109
RESULT 10
US-08-189-256A-4
Sequence 4, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Malliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
transforming Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dana, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

us-09-762-105-14.ini

Mon Dec 16 13:20:23 2002

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 01-MAY-1990
PRIORITY DATE: 31-JAN-1990
PRIOR APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
PRIORITY DATE: 25-AUG-1993
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, James E. 36,252
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQUENCE ANALYSIS:
SEQUENCE LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
US-08-189-256A-4

Query Match
Best Local Similarity 46.9% Score 85.4; DB 2; Length 165;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 67 CAGGATGCGTATATTTCTGGGAGCGA 93
Db 61 CAGGATGCGTATATTTCTGGGAGCGA 87

RESULT 11
Sequence 4, Application US/08193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zuhlenko, Oleg V.
APPLICANT: Kanevski, Ivan
APPLICANT: Carreir, Helaine
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Expressing Recombinant Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dana, Dorcas, Horrell and Skillman
ADDRESS: 1600 Locust Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2907
COMPILED BY: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 08/189,256
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, James E. 36,252
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQUENCE ANALYSIS:
SEQUENCE LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA (genomic)
HYPOTHEtical: NO
ANTI-SENSE: NO
US-09-193-853-4

Query Match
Best Local Similarity 46.9% Score 85.4; DB 4; Length 165;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTCCGCCCGCCGCTCAATGAGATGAGATGAGGCTGCTGGGATTGAGCTGAGGGG 66
Db 1 GCTCCGCCCGCCGCTCAATGAGATGAGATGAGGCTGCTGGGATTGAGCTGAGGGG 60

QY 67 CAGGATGCGTATATTTCTGGGAGCGA 93
Db 61 CAGGATGCGTATATTTCTGGGAGCGA 87

RESULT 12
Sequence 2, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zuhlenko, Oleg V.
APPLICANT: Kanevski, Ivan
APPLICANT: Carreir, Helaine
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Expressing Recombinant Plasmids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dana, Dorcas, Horrell and Skillman
ADDRESS: 1600 Locust Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2907
COMPILED BY: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1990
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA: US 07/518,763
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990

```

```
ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Janet E.
: REGISTRATION NUMBER: 36,252
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-4100
: INFORMATION: (215) 563-4044
: SEQUENCE CHARACTERISTICS:
: LENGTH: 168 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-08-193-853-2

Query Match 46.9%; Score 85.4; DB 2; Length 168;
Best Local Similarity 98.9%; Pred. No. 3.6e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 GCTCCCGCCGCGCTTCATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGG 60

QY 67 CAGGGATGGCTATATTTCTGGGAGGA 93
Db 61 CAGGGATGGCTATATTTCTGGGAGGA 87

RESULT 14
US-09-283-419-3
: Sequence 3; Application US/09283419A
: Patent No. 6218145
: GENERAL INFORMATION:
: APPLICANT: Bogosian, Gregg
: APPLICANT: O'Neill, Julia P.
: TITLE OF INVENTION: Bacterial Expression Systems Based on Plasmid or
: TITLE OF INVENTION: Mitochondrial Promoter Combinations
: REFERENCE NUMBERS:
: CURRENT FILING DATE: 1999-04-03
: EARLIER FILING DATE: 1998-04-02
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 3
: LENGTH: 184
: COUNTRY: USA
: ORGANISM: Nicotiana tabacum
: US-09-283-419-3

Query Match 46.9%; Score 85.4; DB 4; Length 184;
Best Local Similarity 98.9%; Pred. No. 3.7e-20;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2 GCTCCCGCCGCGCTTCATGAGATGATAGAGGCTCGTGGGATTGACGTGAGGGG 61

QY 67 CAGGGATGGCTATATTTCTGGGAGGA 93
Db 62 CAGGGATGGCTATATTTCTGGGAGGA 88

RESULT 15
US-08-189-256A-24
: Sequence 2; Application US/08189256A
: Patent No. 5827713
: GENERAL INFORMATION:
: APPLICANT: Wallig, Pal
: APPLICANT: Svab, Zora
: APPLICANT: Staub, Jeffrey
: APPLICANT: Zoubenko, Oleg V.
: APPLICANT: Allison, Lori A.
: APPLICANT: Carrier, Helaine
: APPLICANT: Kanevski, Ivan
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 01:28:19 : Search time 88 seconds

(without alignments)
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Title: US-09-762-105-14

Perfect score: 182.

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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- 3: /cgn2_6/ptodata/2/pubna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq.*
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- 13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	69.2	38.0	399	9	US-09-813-718-9
4	67.5	37.1	5018	9	US-09-813-718-9
5	66.8	36.7	1057	9	US-09-987-107-51
6	66.8	36.7	1088	9	US-09-987-107-49
7	66.8	36.7	1217	9	US-09-987-107-47
8	66.8	36.7	1238	9	US-09-987-107-53
9	66.8	36.7	1238	9	US-09-987-107-55
10	66.8	36.7	1238	9	US-09-987-107-57
11	66.8	36.7	1238	9	US-09-987-107-59
12	66.8	36.7	1241	9	US-09-987-107-61
13	66.8	36.7	1241	9	US-09-987-107-63
14	66.8	36.7	1241	9	US-09-987-107-65
15	66.8	36.7	1282	9	US-09-987-107-43
16	66.8	36.7	1285	9	US-09-987-107-45
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21 66.4 36.5 5174 9 US-09-813-718-1 Sequence 1, Appli
22 65.6 36.0 4877 9 US-09-813-718-11 Sequence 11, Appli
23 65.4 35.9 656 9 US-09-976-297-5 Sequence 5, Appli
24 65.4 35.9 656 9 US-09-976-297-7 Sequence 7, Appli
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26 65.4 35.9 4811 9 US-09-813-718-13 Sequence 13, Appli
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31 59.6 32.7 5230 10 US-09-953-321-14 Sequence 14, Appli
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41 51.6 28.4 630 10 US-09-929-918-6 Sequence 6, Appli
42 51.6 28.4 5502 9 US-09-736-457-785 Sequence 785, App
43 51.6 28.4 5502 9 US-09-736-457-785 Sequence 785, App
44 51.6 28.4 6353 9 US-09-736-457-784 Sequence 784, App
45 51.6 28.4 6353 9 US-09-736-457-784 Sequence 784, App

ALIGNMENTS

RESULT 1
; Sequence 1, Application US/09843324A
; Patent No. US20020042934A1
; GENERAL INFORMATION:
; INVENTOR: Steven D. Offrey
; APPLICANT: Veda Corporation
; APPLICANT: Broyles, Debra
; TITLE OF INVENTION: Method for the transformation of plant cell plastids
; FILE REFERENCE: 15869/WO
; CURRENT APPLICATION NUMBER: US/09/843,324A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/199,774
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 2
; NOT IN SEQ ID NOS: Patent in version 3.0
; SEQ ID NO. 1
; LENGTH: 202
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-843-324A-1

Query Match 42.7%; Score 77.8; DB 10; Length 202;
Best Local Similarity 97.5%; Ref No. 3, 1e-15;
Matches 79; Conservative 2; Mismatches 0; Gaps 0;
QY 13 CCCCCTCGTTCATGAGATCGATGAGATCGTGGGATTCGACGTAGGCGGCGAGGA 72
Db 11 CCCCCTCGTTCATGAGATCGATGAGATCGTGGGATTCGACGTAGGCGGCGAGGA 70
QY 73 TGGCTATATTCGGGAGGGA 93
Db 71 TGGCTATATTCGGGAGGGA 91
RESULT 2
US-09-843-324A-2
; Sequence 2, Application US/09843324A
; Patent No. US20020042934A1
; GENERAL INFORMATION:

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RESULT 4
US-09-813-718-9
? Application US/09813718
? Publication No. US2002018266A1
? GENERAL INFORMATION:
? APPLICANT: Schimmler, Paul
? APPLICANT INVENTOR(S): Kelschke
? INVENTOR(S) ADDRESS: Hummelrodtstr. 10, 48159 Münster, Germany
? TITLE OF INVENTION: The Regulation of Angiogenesis
? FILE REFERENCE: 00-221
? CURRENT APPLICATION NUMBER: US/09/813,718
? CURRENT FILING DATE: 2001-03-21
? PRIORITY CLAIMING DATE: 2001-03-21
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 9
? LENGTH: 5018
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (3428)..(4879)
? OTHER INFORMATION: Description of Artificial Sequence: human
? SEQUENCE DESCRIPTION: FULL LENGTH TRIPS IN PFZ20B
US-09-813-718-9
Query Match      37.1%   Score 67.6; DB 9; Length 5018;
Best Local Similarity    34.6%   Prefr. 0; Mismatches 12; Indels 0; Gaps 0;
Matches          0; Conservative

QY      89 AGGAGACACCAACGGTGTCCCATGAGAATAATTTGTTTAACCTTAGAAGAGAGAT 148
DB      3364 AAGGAGAGCACACCGGTGTTCCTTGAGAAATATTTGTTTAACCTTAGAAGAGAGAT 3423

QY      149 ACATATTGGCAAGCA 162
DB      3424 ACATATGCCCAACGA 3437

RESULT 5
US-09-987-107-51
? Sequence 51, Application US/09987107
? Patent No. US20020156007A1
? ORGANISM: Homo sapiens
? APPLICANT: GRAVERSEN, Jønes
? APPLICANT: MOESTRUP, Søren
? TITLE OF INVENTION: APOLOPOROTHEIN ANALOGUES
? FILE REFERENCE: 00-221
? CURRENT APPLICATION NUMBER: US/09/987,107
? CURRENT FILING DATE: 2001-11-13
? PRIOR APPLICATION NUMBER: US 60/264,022
? PRIOR FILING DATE: 2001-01-26
? PRIORITY CLAIMING DATE: 2001-01-26
? CURRENT FILING DATE: 2001-01-15
? PRIOR APPLICATION NUMBER: DK PA2000 01682
? PRIOR FILING DATE: 2000-11-10
? NUMBER OF SEQ ID NOS: 91
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 51
? LENGTH: 1057
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (100)..(882)
? OTHER INFORMATION:
? OTHER INFORMATION:
US-09-987-107-51
Query Match      36.7%   Score 66.8; DB 9; Length 1057;
Best Local Similarity    37.1%   Prefr. 0; Mismatches 2; Indels 0; Gaps 0;
Matches          68; Conservative

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Db 36 AGCGAGACACACACGGTTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95
      |||||||
Qy 149 ACATATGGCA 158
      |||||||
Db 96 ACATATGGGA 105
      |||||||

RESULT 6
US-09-987-107-49
; Sequence 49, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; NAME/KEY: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7H6 Trip-A-Apo A-1-del 43 - AmpR plasmid
; NAME/KEY: CDS
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 1217
; TYPE: DNA

Query Match 36.7%; Score 66.8; DB 9; Length 1088;
Best Local Similarity 97.1%; Pred. No. 2.5e-12;
Matches 69; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGCGAGACACACCGTTTCCGACTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148
Db 36 AGCGAGACACACCGTTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95
      |||||||
Qy 149 ACATATGGCA 158
      |||||||
Db 96 ACATATGGGA 105
      |||||||

RESULT 7
US-09-987-107-47
; Sequence 47, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; NAME/KEY: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 1217
; TYPE: DNA

Query Match 36.7%; Score 66.8; DB 9; Length 1088;
Best Local Similarity 97.1%; Pred. No. 2.5e-12;
Matches 69; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGCGAGACACACCGTTTCCGACTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148
Db 36 AGCGAGACACACCGTTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95
      |||||||
Qy 149 ACATATGGCA 158
      |||||||
Db 96 ACATATGGGA 105
      |||||||
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7H6 Trip-A-Apo A-1 - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1047)
; OTHER INFORMATION:
; US-09-987-107-47

Query Match 36.7%; Score 66.8; DB 9; Length 1217;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGCGAGACACACCGTTTCCGACTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148
Db 36 AGCGAGACACACCGTTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95
      |||||||
Qy 149 ACATATGGCA 158
      |||||||
Db 96 ACATATGGGA 105
      |||||||

RESULT 8
US-09-987-107-53
; Sequence 53, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; NAME/KEY: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7H6 Trip-A-Apo A1 K9A K15A - AmpR plasmid
; NAME/KEY: CDS
; LOCATION: (100)..(1047)
; OTHER INFORMATION:
; US-09-987-107-53

Query Match 36.7%; Score 66.8; DB 9; Length 1217;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 89 AGCGAGACACACCGTTTCCGACTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 148
Db 36 AGCGAGACACACCGTTTCCCTCTAGAAATAATTTGTTAACTTTAAGAGGAGATAT 95
      |||||||
Qy 149 ACATATGGCA 158
      |||||||
Db 96 ACATATGGGA 105
      |||||||

RESULT 9
US-09-987-107-55
; Sequence 55, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; NAME/KEY: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
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DB 96 ACATATGGGA 105
US-09-987-107-59
Sequence 59, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
CURRENT APPLICATION NUMBER: US/09/987.107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
FILE REFERENCE: GRAVERSENIA, Jonas
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 1238
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1 Final K9AK15A - AmpR plasmid
NAME/KEY: CDS
LOCATION: (100)..(1068)
OTHER INFORMATION:
US-09-987-107-59
Query Match
Best Local Similarity 36.7%; Score 66.8; DB 9; Length 1238;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 89 AGGAGACACACACGGTTCCCTCTAGAAATAATTTTGAACCTTTAAGAAGAGATAT 148
DB 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTTGAACCTTTAAGAAGAGATAT 95
QY 149 ACATATGGCA 158
DB 96 ACATATGGGA 105
US-09-987-107-61
Sequence 61, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
CURRENT APPLICATION NUMBER: US/09/987.107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
FILE REFERENCE: GRAVERSENIA, Jonas
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
LENGTH: 1241
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: pT7H6 (GS)3 Trip-A-Fn-Apo A1 AmpR plasmid
NAME/KEY: CDS

DB 96 ACATATGGGA 105
US-09-987-107-59
Sequence 59, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
CURRENT APPLICATION NUMBER: US/09/987.107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
FILE REFERENCE: GRAVERSENIA, Jonas
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 1238
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1 - AmpR plasmid
NAME/KEY: CDS
LOCATION: (100)..(1068)
OTHER INFORMATION:
US-09-987-107-59
Query Match
Best Local Similarity 36.7%; Score 66.8; DB 9; Length 1238;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 89 AGGAGACACACACGGTTCCCTCTAGAAATAATTTTGAACCTTTAAGAAGAGATAT 148
DB 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTTGAACCTTTAAGAAGAGATAT 95
QY 149 ACATATGGCA 158
DB 96 ACATATGGGA 105
US-09-987-107-57
Sequence 57, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
CURRENT APPLICATION NUMBER: US/09/987.107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
FILE REFERENCE: GRAVERSENIA, Jonas
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
LENGTH: 1238
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo A1-final - AmpR plasmid
NAME/KEY: CDS
LOCATION: (100)..(1068)
OTHER INFORMATION:
US-09-987-107-57
Query Match
Best Local Similarity 36.7%; Score 66.8; DB 9; Length 1238;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 89 AGGAGACACACACGGTTCCCTCTAGAAATAATTTTGAACCTTTAAGAAGAGATAT 148
DB 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTTGAACCTTTAAGAAGAGATAT 95
QY 149 ACATATGGCA 158

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; LOCATION: (100)..(1071)
; OTHER INFORMATION:
US-09-987-107-61

Query Match      36.7%; Score 66.8; DB 9; Length 1241;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACACACACGGTTCCCACTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 148
    |||||||
Db 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
    |||||||
Db 96 ACATATGGGA 105

RESULT 13
US-09-987-107-63
; Sequence 63, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)..(1071)
; OTHER INFORMATION:
US-09-987-107-63

Query Match      36.7%; Score 66.8; DB 9; Length 1241;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACACACACGGTTCCCACTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 148
    |||||||
Db 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
    |||||||
Db 96 ACATATGGGA 105

RESULT 14
US-09-987-107-65
; Sequence 65, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)..(1107)
; OTHER INFORMATION:
US-09-987-107-65

Query Match      36.7%; Score 66.8; DB 9; Length 1282;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 AGGAGACACACACGGTTCCCACTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 148
    |||||||
Db 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
    |||||||
Db 96 ACATATGGGA 105

RESULT 15
US-09-987-107-43
; Sequence 43, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)..(1107)
; OTHER INFORMATION:
US-09-987-107-43

Query Match      36.7%; Score 66.8; DB 9; Length 1241;
Best Local Similarity 97.1%; Pred. No. 2.6e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

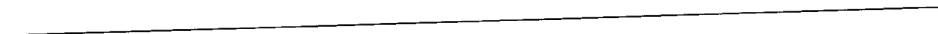
QY 89 AGGAGACACACACGGTTCCCACTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 148
    |||||||
Db 36 AGGAGACACACACGGTTCCCTCTAGAAATAATTTGTTAACTTTAAGAAGGAGATAT 95

QY 149 ACATATGGCA 158
    |||||||
Db 96 ACATATGGGA 105
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us-09-762-105-14.rnpb

Mon Dec 16 13:20:24 2002

Search completed: December 15, 2002, 03:13:31
Job time : 92 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 15, 2002, 00:24:28 ; Search time 2428 Seconds

(without alignments)
1213.994 Million cell updates/sec

Title: US-09-762-105-14

Perfect score: 182

Sequence: 1 gacgtgcctcccccgcctc.....tgcactgtggacaggctacg 182

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_esthum:*

4: em_esthum:*

5: em_esthum:*

6: em_esthum:*

7: em_esthum:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_esthum:*

16: gb_gss:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_fun:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_ric:*

27: em_gss_ric:*

28: em_gss_ric:*

29: em_gss_ric:*

30: em_gss_ric:*

31: em_gss_ric:*

32: em_gss_ric:*

33: em_gss_ric:*

34: em_gss_ric:*

35: em_gss_ric:*

36: em_gss_ric:*

37: em_gss_ric:*

38: em_gss_ric:*

39: em_gss_ric:*

40: em_gss_ric:*

41: em_gss_ric:*

42: em_gss_ric:*

43: em_gss_ric:*

44: em_gss_ric:*

45: em_gss_ric:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72.6	39.9	787	17	BH558942 BOHL272TR
2	72.4	39.8	775	17	BH424823 BOHLN79TR
3	72.2	39.7	735	17	BH509684 BOHS07TF
4	72.2	39.7	838	17	BH472349 BOCIY45TF
5	71.8	39.5	770	17	BH68002 BOMLN95TF
6	71.8	39.5	836	17	BH709230 BONN033TR

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	71.8	39.5	841	17	BH653765
c	71.6	39.3	724	17	BH418480
9	71	39.0	805	17	BH474481
c	71	39.0	847	17	BOHY09TR
11	70.8	38.9	169	17	BH721450
12	70.8	38.9	199	17	BOFM11TR
13	70.8	38.9	238	17	AQ62940
14	70.8	38.9	258	17	LERG14TR
c	70.8	38.9	305	17	BH537952
15	70.8	38.9	325	17	BOGFO3TR
16	70.8	38.9	332	17	BOGFO3TR
17	70.8	38.9	367	17	BH577593
18	70.8	38.9	368	17	BOGFO3TR
19	70.8	38.9	416	17	BOGFO3TR
20	70.8	38.9	419	17	BOGFO3TR
21	70.8	38.9	422	17	BOGFO3TR
22	70.8	38.9	423	17	BOGFO3TR
23	70.8	38.9	434	17	BOGFO3TR
24	70.8	38.9	435	17	BOGFO3TR
25	70.8	38.9	441	17	BOGFO3TR
26	70.8	38.9	448	17	BOGFO3TR
27	70.8	38.9	450	17	BOGFO3TR
28	70.8	38.9	451	17	BOGFO3TR
29	70.8	38.9	459	17	BOGFO3TR
30	70.8	38.9	466	17	BOGFO3TR
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32	70.8	38.9	469	17	BOGFO3TR
c	70.8	38.9	475	17	BOGFO3TR
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c	70.8	38.9	482	17	BOGFO3TR
35	70.8	38.9	484	17	BOGFO3TR
36	70.8	38.9	487	17	BOGFO3TR
37	70.8	38.9	488	17	BOGFO3TR
38	70.8	38.9	497	17	BOGFO3TR
39	70.8	38.9	501	17	BOGFO3TR
40	70.8	38.9	503	17	BOGFO3TR
41	70.8	38.9	507	17	BOGFO3TR
42	70.8	38.9	507	17	BOGFO3TR
43	70.8	38.9	508	17	BOGFO3TR
44	70.8	38.9	508	17	BOGFO3TR
c	70.8	38.9	511	17	BOGFO3TR

ALIGNMENTS

RESULT 1	787 bp	DNA	linear	GSS 14-DEC-2001
BH558942	BOHL272TR	BOHL Brassica oleracea genomic clone BOHL272, DNA		
Locus	sequence			
DEFINITION	BH558942.1	GI:17810722		
ACCESSION	BH558942			
VERSION	BH558942.1			
KEYWORDS	GSS.			
SOURCE	Brassica oleracea.			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Eudicotyledons; Eudicotyledons; Rosales; Brassicales; Brassicaceae; Brassica.			
REFERENCE	1 (bases 1 to 787)			
AUTHORS	Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.			
TITLE	Whole genome shotgun sequencing of Brassica oleracea			
JOURNAL	Unpublished (2001)			
COMMENT	Other_GSSs: BOHL272TF			
	Contact: Chris Town			
	TIGR			
	TIGR Medical Center Drive, Rockville, MD 20850, USA.			
	Telex: 301-838-3523			
	Fax: 301-838-0208			
	Email: cdtown@tigr.org			
	DNA is from a doubled haploid provided by Tom Osborn.			
	Seq primer: TR			
	Class: sheared ends.			
	Location/Qualifiers			
	1. 787			

source

[illegible]

[illegible]

AUTHORS	TITLE	JOURNAL	COMMENT
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterback, T., Feldblum, J., Liao, F., Cressy, T., and Fraser, C.W.	Genomic survey sequencing of <i>Landsberg erecta</i> ecotype of <i>Arabidopsis thaliana</i> and identification of sequence-based polymorphisms	Unpublished (2000)	Contact: Xiaoying Lin The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: xtl@igmr.org For additional information, see http://www.tigr.org/tdb/at/at.html Similar to A. thaliana chloroplast sequence (GB:AF000423) Seq primer: TR Class: shotgun.
FEATURES	source	Location/Qualifiers	
	1. .169	/organism="Arabidopsis thaliana" /strain="Landsberg erecta" /db_xref="taxon:3702" /clone="LEGI43" /clone-lib="LEGI" /note="organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 kbp before ligation."	
BASE COUNT	46 a	49 c	27 g 47 t
ORIGIN	Query Match	Best Local Similarity	Matches
	38-9%; Score 70.8; DB 17; Length 169;	86.7%; Pred. No. Se-14; Indels 0; Gaps 0;	
	Matches: 78; Conservative 0; Mismatches 12;		
QY 4	CTGTCGCCCGCCGTCGTCATGAGTAAGAGCGCTGCGGATGACGTGAGG 63		
Db 161	CTTGTCTCCCTCCGCTGTCATGAATGAAGAGCGCTGCGGATGACGTGAGG 102		
QY 64	GGGAGGAGTGCGTATATTCTGGGAGGA 93		
Db 101	GGGTAGGGGTAGCTATATTCTGGGAGGA 72		
RESULT 12	BH537952	199 bp DNA linear	GSS 14-Dec-2001
LOCUS	BH537952	BOGF Brassica oleracea genomic clone BOGFU38, DNA	
DEFINITION	BOGFU38TKR BOGF Brassica oleracea genomic clone BOGFU38, DNA sequence.		
ACCESSION	BH537952		
VERSION	BH537952.1	GI:17776124	
KEYWORDS	GSS		
SOURCE	Brassica oleracea		
ORGANISM	Brassica oleracea		
REFERENCE	1 (bases 1 to 199)		
AUTHORS	Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.		
TITLE	Whole genome shotgun sequencing of Brassica oleracea		
JOURNAL	Unpublished (2001)		
COMMENT	Other_GSSs: BOGFU38TKR Contact: Chris Town TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR Class: sheared ends.		
FEATURES	source	Location/Qualifiers	
	1. .199	/organism="Brassica oleracea" /strain="TO1000DH3" /db_xref="taxon:3712"	

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/clone="BOGRU38"
/clone.lib="BOGR"
/note="vector: pBOS1: Site_1: BatX1: 2-3 kb sheared
genomic DNA inserted into pBOS1 using BstXI linkers"
53 a 34 c 57 c
OY 38.9%; Score 70.8; DB 17; Length 199;
Best Match Similarity 86.7%; Pred. No. 5,3e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
4 CTCGCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCGTGGATTGACGTGAGG 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 58 CTTGCTCCCTCCGCTGTGATCGAATAGATGATAGAGGCTGTGGATTGACGTGAG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 64 GCGAGGATGGCTATATCTCGSGAGGA 93
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 118 GCGTAGGGGTAGCTATATTTCTGGGCGCA 147
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
SUMMARY
757595
LOCUS
BOCM49TR BO_2_3_KB Brassica oleracea genomic clone BOCM49, DNA
sequence.
1867535
BH675595.1 GI:18748038
GSS.
SOURCE
Brassica oleracea.
ORGANISM
Brassica oleracea
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosidiales; eudicots II; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eudicots II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 238)
Tow, C.D., Van Aken, S., Utterback, T., and Fraser, C.M.
Molecular cloning and sequencing of Brassica oleracea
cDNA library. Submitted (2001)
Unpublished
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-0208
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: 476 ends.
Class: Structural
Location/Qualifiers
1..238
location="Brassica oleracea"
/strain="OL000003"
/clone="BOCM49"
/note="vector: pBOS1: Site_1: BatX1: 2-3 kb sheared
genomic DNA inserted into pBOS1 using BstXI linkers"
63 a 41 c 67 c 67 c
OY 38.9%; Score 70.8; DB 17; Length 238;
Best Match Similarity 86.7%; Pred. No. 5,3e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
4 CTCGCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCGTGGATTGACGTGAGG 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 99 CTTGCTCCCTCCGCTGTGATCGAATAGATGATAGAGGCTGTGGATTGACGTGAGG 158
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 64 GCGAGGATGGCTATATCTCGSGAGGA 93
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 159 GCGTAGGGGTAGCTATATTTCTGGGCGCA 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

FEATURES
..source
1..238
location="Brassica oleracea"
/strain="OL000003"
/clone="BOCM49"
/note="vector: pBOS1: Site_1: BatX1: 2-3 kb sheared
genomic DNA inserted into pBOS1 using BstXI linkers"
63 a 41 c 67 c 67 c
OY 38.9%; Score 70.8; DB 17; Length 238;
Best Match Similarity 86.7%; Pred. No. 5,3e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
4 CTCGCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCGTGGATTGACGTGAGG 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 99 CTTGCTCCCTCCGCTGTGATCGAATAGATGATAGAGGCTGTGGATTGACGTGAGG 158
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 64 GCGAGGATGGCTATATCTCGSGAGGA 93
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 159 GCGTAGGGGTAGCTATATTTCTGGGCGCA 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
SUMMARY
757595
LOCUS
BOCM49TR BO_2_3_KB Brassica oleracea genomic clone BOCM49, DNA
sequence.
1867535
BH675595.1 GI:18748038
GSS.
SOURCE
Brassica oleracea.
ORGANISM
Brassica oleracea
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosidiales; eudicots II; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eudicots II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 238)
Tow, C.D., Van Aken, S., Utterback, T., and Fraser, C.M.
Molecular cloning and sequencing of Brassica oleracea
cDNA library. Submitted (2001)
Unpublished
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-0208
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: 476 ends.
Class: Structural
Location/Qualifiers
1..238
location="Brassica oleracea"
/strain="OL000003"
/clone="BOCM49"
/note="vector: pBOS1: Site_1: BatX1: 2-3 kb sheared
genomic DNA inserted into pBOS1 using BstXI linkers"
63 a 41 c 67 c 67 c
OY 38.9%; Score 70.8; DB 17; Length 238;
Best Match Similarity 86.7%; Pred. No. 5,3e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
4 CTCGCTCCCGCCGCTGCTCAATGAGATGGATAGAGGCTCGTGGATTGACGTGAGG 58
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 99 CTTGCTCCCTCCGCTGTGATCGAATAGATGATAGAGGCTGTGGATTGACGTGAGG 158
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 64 GCGAGGATGGCTATATCTCGSGAGGA 93
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 159 GCGTAGGGGTAGCTATATTTCTGGGCGCA 188
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